Supplemental Amendment/Response for application 10/037, 718 Applicants MCGINNIS ET AL. 12 November 20, 2005; 26 total pages submitted by fax to 571-273-8300

In the Abstract

Please amend the Abstract by replacing the current Abstract with the new Abstract on the next page.

Abstract

Invention versions are techniques (methods, software, apparatuses, oligonucleotides) for new linkage studies (and associated genotyping) using bi-allelic (or equivalent) markers (e.g., SNPs) that increase the power (and efficiency) of association-based linkage tests (and studies) to detect linkage. Each marker and trait-causing polymorphism is described as located at a point on a two-dimensional map (like an x-y graph) having the dimensions of chromosomal location and least common allele frequency. The techniques increase power by promoting the occurrence of the conditions of a positively associated marker allele and trait-causing polymorphism allele having allele frequencies of similar magnitude by choosing markers so one or more markers is within a small two-dimensional distance of each point in a map region consisting of one or more points. Some regions are confined to an allele frequency subrange. Increased power results when a trait-causing polymorphism is located at a point in the region with the conditions present.